RAW SEQUENCE LISTING
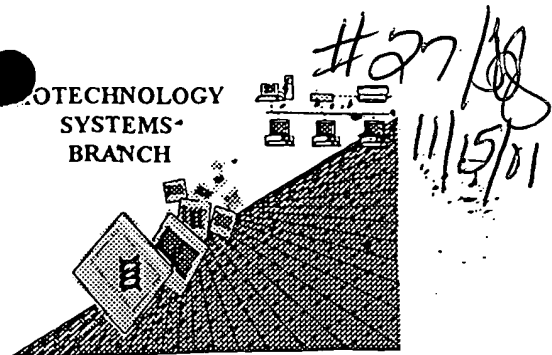## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

RECEIVED

NOV 1 3 2001

Application Serial Number: _09/042 488_

Source: _OIPE_

Date Processed by STIC: _09/18/2001_

TECH CENTER 1600/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/042 488

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWA:

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length.

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 . ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

```
RAW SEQUENCE LISTING              DATE: 09/18/2001
PATENT APPLICATION:  US/09/042,488   TIME: 10:29:45

     Input Set : A:\Sal520-2.app
     Output Set: N:\CRF3\09182001\I042488.raw
```

```
      3 <110> APPLICANT: EVANS, RONALD M.
      4       NO, DAVID
      5       SAEZ, ENRIQUE
      7 <120> TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
      8       MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO
     10 <130> FILE REFERENCE: SALK1520-2
     12 <140> CURRENT APPLICATION NUMBER: 09/042,488
C--> 13 <141> CURRENT FILING DATE: 2001-08-29
     15 <150> PRIOR APPLICATION NUMBER: 08/974,530
     16 <151> PRIOR FILING DATE: 1997-11-19
     18 <150> PRIOR APPLICATION NUMBER: 08/628,830
     19 <151> PRIOR FILING DATE: 1996-04-05
     21 <160> NUMBER OF SEQ ID NOS: 18
     23 <170> SOFTWARE: PatentIn Ver. 2.1
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 71
     27 <212> TYPE: PRT
     28 <213> ORGANISM: Artificial Sequence
     30 <220> FEATURE:
     31 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
     32       peptide sequence
     34 <220> FEATURE:
     35 <221> NAME/KEY: MOD_RES
     36 <222> LOCATION: (2)..(3)
     37 <223> OTHER INFORMATION: Any amino acid
     39 <220> FEATURE:
     40 <221> NAME/KEY: MOD_RES
     41 <222> LOCATION: (5)..(6)
     42 <223> OTHER INFORMATION: Any amino acid
     44 <220> FEATURE:
     45 <221> NAME/KEY: MOD_RES
     46 <222> LOCATION: (8)
     47 <223> OTHER INFORMATION: Any amino acid
     49 <220> FEATURE:
     50 <221> NAME/KEY: MOD_RES
     51 <222> LOCATION: (10)
     52 <223> OTHER INFORMATION: Any amino acid
     54 <220> FEATURE:
     55 <221> NAME/KEY: MOD_RES
     56 <222> LOCATION: (12)
     57 <223> OTHER INFORMATION: Any amino acid
     59 <220> FEATURE:
     60 <221> NAME/KEY: MOD_RES
     61 <222> LOCATION: (14)..(17)
     62 <223> OTHER INFORMATION: Any amino acid
     64 <220> FEATURE:
     65 <221> NAME/KEY: MOD_RES
```

Does Not Comply
Corrected Diskette Needed

```
 66 <222> LOCATION: (19)..(20)
 67 <223> OTHER INFORMATION: Any amino acid
 69 <220> FEATURE:
 70 <221> NAME/KEY: MOD_RES
 71 <222> LOCATION: (23)
 72 <223> OTHER INFORMATION: Any amino acid
 74 <220> FEATURE:
 75 <221> NAME/KEY: MOD_RES
 76 <222> LOCATION: (26)
 77 <223> OTHER INFORMATION: Any amino acid
 79 <220> FEATURE:
 80 <221> NAME/KEY: MOD_RES
 81 <222> LOCATION: (28)..(38)
 82 <223> OTHER INFORMATION: Any amino acid
 84 <220> FEATURE:
 85 <221> NAME/KEY: MOD_RES
 86 <222> LOCATION: (40)..(47)
 87 <223> OTHER INFORMATION: Any amino acid
 89 <220> FEATURE:
 90 <221> NAME/KEY: MOD_RES
 91 <222> LOCATION: (49)..(51)
 92 <223> OTHER INFORMATION: Any amino acid
 94 <220> FEATURE:
 95 <221> NAME/KEY: MOD_RES
 96 <222> LOCATION: (53)..(54)
 97 <223> OTHER INFORMATION: Amny amino acid
 99 <220> FEATURE:
100 <221> NAME/KEY: MOD_RES
101 <222> LOCATION: (56)..(57)
102 <223> OTHER INFORMATION: Any amino acid
104 <220> FEATURE:
105 <221> NAME/KEY: MOD_RES
106 <222> LOCATION: (59)..(60)
107 <223> OTHER INFORMATION: Any amino acid
109 <220> FEATURE:
110 <221> NAME/KEY: MOD_RES
111 <222> LOCATION: (63)..(64)
112 <223> OTHER INFORMATION: Any amino acid
114 <220> FEATURE:
115 <221> NAME/KEY: MOD_RES
116 <222> LOCATION: (67)..(69)
117 <223> OTHER INFORMATION: Any amino acid
119 <400> SEQUENCE: 1
W--> 120 Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
     121  1               5                  10                  15
W--> 123 Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
     124              20                  25                  30
W--> 126 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
     127              35                  40                  45
```

Input Set : A:\Sa1520-2.app
Output Set: N:\CRF3\09182001\I042488.raw

```
W--> 129  Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
     130       50               55              60
W--> 132  Lys Cys Xaa Xaa Xaa Gly Met
     133   65               70
     136  <210> SEQ ID NO: 2
     137  <211> LENGTH: 5
     138  <212> TYPE: PRT
     139  <213> ORGANISM: Artificial Sequence
     141  <220> FEATURE:
     142  <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     143        peptide
     145  <400> SEQUENCE: 2
     146  Glu Gly Cys Lys Gly
     147   1               5
     150  <210> SEQ ID NO: 3
     151  <211> LENGTH: 5
     152  <212> TYPE: PRT
     153  <213> ORGANISM: Artificial Sequence
     155  <220> FEATURE:
     156  <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
     157        peptide
     159  <400> SEQUENCE: 3
     160  Gly Ser Cys Lys Val
     161   1               5
     164  <210> SEQ ID NO: 4
     165  <211> LENGTH: 2241
     166  <212> TYPE: DNA
     167  <213> ORGANISM: Artificial Sequence
     169  <220> FEATURE:
     170  <223> OTHER INFORMATION: Description of Artificial Sequence: Recombinant
     171        VgEcR
     173  <220> FEATURE:
     174  <221> NAME/KEY: CDS
     175  <222> LOCATION: (1)..(2238)
     177  <400> SEQUENCE: 4
     178  atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac   48
     179  Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
     180   1               5                  10                  15
     182  ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat   96
     183  Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
     184           20                  25                  30
     186  ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc  144
     187  Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
     188        35                  40                  45
     190  cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt  192
     191  His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
     192        50                  55                  60
     194  gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag  240
     195  Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
```

[Handwritten annotations:] Synthetic Peptide is not a sufficient response to describe or explain your artificial sequence

```
196  65                    70                   75                   80
198 ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc   288
199 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
200                   85                   90                   95
202 gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa   336
203 Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
204                   100                  105                  110
206 agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa   384
207 Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
208          115                  120                  125
210 gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac   432
211 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
212      130                  135                  140
214 aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt   480
215 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
216 145                  150                  155                  160
218 acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg   528
219 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
220                  165                  170                  175
222 gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc   576
223 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
224              180                  185                  190
226 ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt   624
227 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
228          195                  200                  205
230 gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg   672
231 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
232      210                  215                  220
234 acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct   720
235 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
236 225                  230                  235                  240
238 ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca   768
239 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
240                  245                  250                  255
242 tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata   816
243 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
244              260                  265                  270
246 ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag   864
247 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
248          275                  280                  285
250 ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag   912
251 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
252      290                  295                  300
254 cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac   960
255 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
256 305                  310                  315                  320
258 gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata  1008
259 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
260                  325                  330                  335
```

```
262 ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt    1056
263 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
264         340             345             350
266 aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg    1104
267 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
268         355             360             365
270 tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg    1152
271 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
272     370             375             380
274 gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac    1200
275 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
276 385             390             395             400
278 aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc    1248
279 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
280             405             410             415
282 cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc    1296
283 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
284         420             425             430
286 act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa    1344
287 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
288         435             440             445
290 cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat    1392
291 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
292     450             455             460
294 ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca    1440
295 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
296 465             470             475             480
298 aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac    1488
299 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
300             485             490             495
302 gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag    1536
303 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
304         500             505             510
306 ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag    1584
307 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
308         515             520             525
310 tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct    1632
311 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
312     530             535             540
314 gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat    1680
315 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
316 545             550             555             560
318 tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag    1728
319 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
320             565             570             575
322 cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat    1776
323 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
324         580             585             590
326 tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag    1824
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/042,488

DATE: 09/18/2001
TIME: 10:29:47

Input Set : A:\Sa1520-2.app
Output Set: N:\CRF3\09182001\I042488.raw

```
L:13   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:120  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:126  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:129  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:132  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
```

a/zC Cmlearhod Slue Amby

Examiner Kaushal -

Do you know if a CRF is coming? If the applicant hasn't sent the information, your docket clerk needs to see if new disks were sent in, and if not, we should go ahead and cancel this search request. You can always put in a new request when the CRF becomes availible.

Caryn S. Wesner-Early, MSLS
Technical Information Specialist
Biotechnology and Chemical Library
U.S. Patent and Trademark Office
Phone: (703) 308-4501
Fax: (703) 308-4496
caryn.wesner@uspto.gov

-----Original Message-----
From: Kaushal, Sumesh
Sent: Tuesday, September 18, 2001 2:12 PM
To: Wesner-Early, Caryn
Subject: FW: Re: 09/042,488

Please hold the search till STC forward CRF
thanks
-sumesh

-----Original Message-----
From: Spencer, Mark
Sent: Tuesday, September 18, 2001 01:56 PM
To: Kaushal, Sumesh
Subject: RE: Re: 09/042,488

Sumesh,
The STIC has not been forwarded a CRF for this SN at this time.

Mark

-----Original Message-----
From: Kaushal, Sumesh
Sent: Friday, September 14, 2001 10:27 AM
To: Spencer, Mark
Subject: FW: Re: 09/042,488

Please note, the SEQ disk for 09/042,488 was recieved on 08/29/01.
Please let me know when STIC would be able to use the SEQ-database for search.
Thanks
Sumesh Kaushal
CM1 12A07 AU1633
Ph: 703-305-6838

1

Examiner Kaushal -

We are unable to process the search request for SN 09/042,488 because there is a problem with the CRF data for this case. If there is a related case that should be used, please let us know. We cannot process this request until valid data is available. Please contact me directly on this - I will hold onto your request until I hear from you. Thanks.

Caryn S. Wesner-Early, MSLS
Technical Information Specialist
Biotechnology and Chemical Library
U.S. Patent and Trademark Office
Phone: (703) 308-4501
Fax: (703) 308-4496
caryn.wesner@uspto.gov